```
RAW SEQUENCE LISTING              DATE: 08/30/2004
PATENT APPLICATION:  US/10/763,692      TIME: 14:40:09

Input Set : N:\Crf3\RULE60\10763692.raw.txt
Output Set: N:\CRF4\08302004\J763692.raw
```

```
 1 <110> APPLICANT: Kennedy, Giulia C.
 2 <120> TITLE OF INVENTION: Polynucleotides Differentially Expressed
 3       in Adenocarcinomas, Polypeptides Encoded Thereby, and
 4       Methods of Use Thereof
 5 <130> FILE REFERENCE: 2300-1575
 6 <140> CURRENT APPLICATION NUMBER: US/10/763,692
 7 <141> CURRENT FILING DATE: 2004-01-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/626,301
 9 <151> PRIOR FILING DATE: 2000-07-25
10 <150> PRIOR APPLICATION NUMBER: 60/145,612
11 <151> PRIOR FILING DATE: 1999-07-26
12 <150> PRIOR APPLICATION NUMBER: 60/148,936
13 <151> PRIOR FILING DATE: 1999-08-13
14 <160> NUMBER OF SEQ ID NOS: 19
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 4612
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo Sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (698)...(3862)
24 <400> SEQUENCE: 1
25     atagcacgac tgtgtatgct ctggaggact gaaaggctgt acaagcccta tgtatttttt      60
26     ttcaaatata catatgcatg ggtcttgctg ctgcctcttt tgctgactgt aattggactt     120
27     tgaagcttcg aagttatatc ataaaaattt gtaacctttg tctgagagag agctcagcta     180
28     agcaatcact ttccacttct tttcacagga taatataaac gtttttcttga aagcttgtga     240
29     acagattgga ttgaaagaag cccagctttt ccatcctgga gatctacagg atttatcaaa     300
30     tcgagtcact gtcaagcaag aagagactga caggagagtg aaaaatgttt tgataacatt     360
31     gtactggctg ggaagaaaag cacaaagcaa cccgtactat aatggtcccc atcttaattt     420
32     gaaagcgttt gagaatcttt taggacaagc actgacgaag gcactcgaag actccagctt     480
33     cctgaaaaga agtggcaggg acagtggcta cggtgacatc tggtgtcctg aacgtggaga     540
34     atttcttgct cctccaaggc accataagag agaagattcc tttgaaagct tggactcttt     600
35     gggctcgagg tcattgacaa gctgctcctc tgatatcacg ttgagagggg ggcgtgaagg     660
36     ttttgaaagt gacacagatt cggaatttac attcaag atg cag gat tat aat aaa      715
37                                             Met Gln Asp Tyr Asn Lys
38                                             1               5
39     gat gat atg tcg tat cga agg att tcg gct gtt gag cca aag act gcg      763
40     Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu Pro Lys Thr Ala
41                 10              15              20
42     tta ccc ttc aat cgt ttt tta ccc aac aaa agt aga cag cca tcc tat      811
43     Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg Gln Pro Ser Tyr
44                 25              30              35
```

RAW SEQUENCE LISTING   DATE: 08/30/2004
PATENT APPLICATION: US/10/763,692   TIME: 14:40:09

Input Set : N:\Crf3\RULE60\10763692.raw.txt
Output Set: N:\CRF4\08302004\J763692.raw

```
45    gta cca gca cct ctg aga aag aaa aag cca gac aaa cat gag gat aac        859
46    Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys His Glu Asp Asn
47         40                  45                  50
48    aga aga agt tgg gca agc ccg gtt tat aca gaa gca gat gga aca ttt        907
49    Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala Asp Gly Thr Phe
50     55                  60                  65                  70
51    tca agg agt aag tcc atg agt gat gtc agc gca gaa gat gtt caa aac        955
52    Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu Asp Val Gln Asn
53                     75              80                  85
54    ttg cgt cag ctg cgt tac gag gag atg cag aaa ata aaa tca caa tta       1003
55    Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile Lys Ser Gln Leu
56                 90                  95                 100
57    aaa gaa caa gat cag aaa tgg cag gat gac ctt gca aaa tgg aaa gat       1051
58    Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp
59             105                 110                 115
60    cgt cga aaa agt tac act tca gat ctg cag aag aaa aaa gaa gag aga       1099
61    Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys Lys Lys Glu Glu Arg
62         120                 125                 130
63    gaa gaa att gaa aag cag gca ctt gag aag tct aag aga agc tct aag       1147
64    Glu Glu Ile Glu Lys Gln Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys
65    135                 140                 145                 150
66    acg ttt aag gaa atg ctg cag gac agg gaa tcc caa aat caa aag tct       1195
67    Thr Phe Lys Glu Met Leu Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser
68                 155                 160                 165
69    aca gtt ccg tca aga agg aga atg tat tct ttt gat gat gtg ctg gag       1243
70    Thr Val Pro Ser Arg Arg Arg Met Tyr Ser Phe Asp Asp Val Leu Glu
71                 170                 175                 180
72    gaa gga aag cga ccc cct aca atg act gtg tca gaa gca agt tac cag       1291
73    Glu Gly Lys Arg Pro Pro Thr Met Thr Val Ser Glu Ala Ser Tyr Gln
74             185                 190                 195
75    agt gag aga gta gaa gag aag gga gca act tat cct tca gaa att ccc       1339
76    Ser Glu Arg Val Glu Glu Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro
77         200                 205                 210
78    aaa gaa gat tct acc act ttt gca aaa aga gag gac cgt gta aca act       1387
79    Lys Glu Asp Ser Thr Thr Phe Ala Lys Arg Glu Asp Arg Val Thr Thr
80    215                 220                 225                 230
81    gaa att cag ctt cct tct caa agt cct gtg gaa gaa caa agc cca gcc       1435
82    Glu Ile Gln Leu Pro Ser Gln Ser Pro Val Glu Glu Gln Ser Pro Ala
83                 235                 240                 245
84    tct ttg tct tct ctg cgt tca cgg agc aca caa atg gaa tca act cgt       1483
85    Ser Leu Ser Ser Leu Arg Ser Arg Ser Thr Gln Met Glu Ser Thr Arg
86             250                 255                 260
87    gtt tca gct tct ctc ccc aga agt tac cgg aaa act gat aca gtc agg       1531
88    Val Ser Ala Ser Leu Pro Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg
89             265                 270                 275
90    tta aca tct gtg gtc aca cca aga ccc ttt ggc tct cag aca agg gga       1579
91    Leu Thr Ser Val Val Thr Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly
92         280                 285                 290
93    atc tca tca ctc ccc aga tct tac acg atg gat gat gct tgg aag tat       1627
```

RAW SEQUENCE LISTING   DATE: 08/30/2004
PATENT APPLICATION: US/10/763,692   TIME: 14:40:09

Input Set : N:\Crf3\RULE60\10763692.raw.txt
Output Set: N:\CRF4\08302004\J763692.raw

```
 94      Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr
 95      295                 300             305                 310
 96      aat gga gat gtt gaa gac att aag aga act cca aac aat gtg gtc agc      1675
 97      Asn Gly Asp Val Glu Asp Ile Lys Arg Thr Pro Asn Asn Val Val Ser
 98                          315             320                 325
 99      acc cct gca cca agc ccg gac gca agc caa ctg gct tca agc tta tct      1723
100      Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln Leu Ala Ser Ser Leu Ser
101                      330             335                 340
102      agc cag aaa gag gta gca gca aca gaa gaa gat gtg aca agg ctg ccc      1771
103      Ser Gln Lys Glu Val Ala Ala Thr Glu Glu Asp Val Thr Arg Leu Pro
104                  345             350                 355
105      tct cct aca tcc ccc ttc tca tct ctt tcc caa gac cag gct gcc act      1819
106      Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser Gln Asp Gln Ala Ala Thr
107              360             365             370
108      tct aaa gcc aca ttg tct tcc aca tct ggt ctt gat tta atg tct gaa      1867
109      Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly Leu Asp Leu Met Ser Glu
110      375                 380                 385                 390
111      tct gga gaa ggg gaa atc tcc cca caa aga gaa gtc tca aga tcc cag      1915
112      Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg Glu Val Ser Arg Ser Gln
113                      395             400                 405
114      gat cag ttc agt gat atg aga atc agc ata aac cag acg cct ggg aag      1963
115      Asp Gln Phe Ser Asp Met Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys
116                  410             415                 420
117      agt ctt gac ttt ggg ttt aca ata aaa tgg gat att cct ggg atc ttc      2011
118      Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe
119                  425             430                 435
120      gta gca tca gtt gaa gca ggt agc cca gca gaa ttt tct cag cta caa      2059
121      Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln
122              440             445             450
123      gta gat gat gaa att att gct att aac aac acc aag ttt tca tat aac      2107
124      Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn
125      455                 460             465                 470
126      gat tca aaa gag tgg gag gaa gcc atg gct aag gct caa gaa act gga      2155
127      Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys Ala Gln Glu Thr Gly
128                      475             480                 485
129      cac cta gtg atg gat gtg agg cgc tat gga aag gct ggt tca cct gaa      2203
130      His Leu Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu
131                  490             495                 500
132      aca aag tgg att gat gca act tct gga att tac aac tca gaa aaa tct      2251
133      Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser
134                  505             510                 515
135      tca aat cta tct gta aca act gat ttc tcc gaa agc ctt cag agt tct      2299
136      Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser
137              520             525             530
138      aat att gaa tcc aaa gaa atc aat gga att cat gat gaa agc aat gct      2347
139      Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His Asp Glu Ser Asn Ala
140      535                 540             545                 550
141      ttt gaa tca aaa gca tct gaa tcc att tct ttg aaa aac tta aaa agg      2395
142      Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu Lys Asn Leu Lys Arg
```

```
143                   555                 560                 565
144      cga tca caa ttt ttt gaa caa gga agc tct gat tcg gtg gtt cct gat     2443
145      Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp Ser Val Val Pro Asp
146                   570                 575                 580
147      ctt cca gtt cca acc atc agt gcc ccg agt cgc tgg gtg tgg gat caa     2491
148      Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg Trp Val Trp Asp Gln
149                   585                 590                 595
150      gag gag gag cgg aag cgg cag gag agg tgg cag aag gag cag gac cgc     2539
151      Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln Lys Glu Gln Asp Arg
152                   600                 605                 610
153      cta ctg cag gaa aaa tat caa cgt gag cag gag aaa ctg agg gaa gag     2587
154      Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu Lys Leu Arg Glu Glu
155      615                 620                 625                 630
156      tgg caa agg gcc aaa cag gag gca gag aga gag aat tcc aag tac ttg     2635
157      Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu Asn Ser Lys Tyr Leu
158                   635                 640                 645
159      gat gag gaa ctg atg gtc cta agc tca aac agc atg tct ctg acc aca     2683
160      Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser Met Ser Leu Thr Thr
161                   650                 655                 660
162      cgg gag ccc tct ctt gcc acc tgg gaa gct acc tgg agt gaa ggg tcc     2731
163      Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr Trp Ser Glu Gly Ser
164                   665                 670                 675
165      aag tct tca gac aga gaa gga acc cga gca gga gaa gag gag agg aga     2779
166      Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly Glu Glu Glu Arg Arg
167                   680                 685                 690
168      cag cca caa gag gaa gtt gtt cat gag gac caa gga aag aag ccg cag     2827
169      Gln Pro Gln Glu Glu Val Val His Glu Asp Gln Gly Lys Lys Pro Gln
170      695                 700                 705                 710
171      gat cag ctt gtt att gag aga gag agg aaa tgg gag caa cag ctt cag     2875
172      Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp Glu Gln Gln Leu Gln
173                   715                 720                 725
174      gaa gag caa gag caa aag cgg ctt cag gct gag gct gag gag cag aag     2923
175      Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu Ala Glu Glu Gln Lys
176                   730                 735                 740
177      cgt cct gcg gag gag cag aag cgc cag gca gag ata gag cgg gaa aca     2971
178      Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr
179                   745                 750                 755
180      tca gtc aga ata tac cag tac agg agg cct gtt gat tcc tat gat ata     3019
181      Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile
182      760                 765                 770
183      cca aag aca gaa gaa gca tct tca ggt ttt ctt cct ggt gac agg aat     3067
184      Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn
185      775                 780                 785                 790
186      aaa tcc aga tct act act gaa ctg gat gat tac tcc aca aat aaa aat     3115
187      Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn
188                   795                 800                 805
189      gga aac aat aaa tat tta gac caa att ggg aac acg acc tct tca cag     3163
190      Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn Thr Thr Ser Ser Gln
191                   810                 815                 820
```

```
192   agg aga tcc aag aaa gaa caa gta cca tca gga gca gaa ttg gag agg      3211
193   Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly Ala Glu Leu Glu Arg
194           825                 830                 835
195   caa caa atc ctt cag gaa atg agg aag aga aca ccc ctt cac aat gac      3259
196   Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr Pro Leu His Asn Asp
197           840                 845                 850
198   aac agc tgg atc cga cag cgc agt gcc agt gtc aac aaa gag cct gtt      3307
199   Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val Asn Lys Glu Pro Val
200   855                 860                 865                 870
201   agt ctt cct ggg atc atg aga aga ggc gaa tct tta gat aac ctg gac      3355
202   Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp
203                       875                 880                 885
204   tcc ccc cga tcc aat tct tgg aga cag cct cct tgg ctc aat cag ccc      3403
205   Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro
206                       890                 895                 900
207   aca gga ttc tat gct tct tcc tct gtg caa gac ttt agt cgc cca cca      3451
208   Thr Gly Phe Tyr Ala Ser Ser Ser Val Gln Asp Phe Ser Arg Pro Pro
209           905                 910                 915
210   cct cag ctg gtg tcc aca tca aac cgt gcc tac atg cgg aac ccc tcc      3499
211   Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser
212           920                 925                 930
213   tcc agc gtg ccc cca cct tca gct ggc tcc gtg aag acc tcc acc aca      3547
214   Ser Ser Val Pro Pro Pro Ser Ala Gly Ser Val Lys Thr Ser Thr Thr
215   935                 940                 945                 950
216   ggt gtg gcc acc aca cag tcc ccc acc ccg aga agc cat tcc cct tca      3595
217   Gly Val Ala Thr Thr Gln Ser Pro Thr Pro Arg Ser His Ser Pro Ser
218                       955                 960                 965
219   gct tca cag tca ggc tct cag ctg cgt aac agg tca gtc agt ggg aag      3643
220   Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn Arg Ser Val Ser Gly Lys
221           970                 975                 980
222   cgc ata tgc tcc tac tgc aat aac att ctg ggc aaa gga gcc gcc atg      3691
223   Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu Gly Lys Gly Ala Ala Met
224           985                 990                 995
225   atc atc gag tcc ctg ggt ctt tgt tat cat ttg cat tgt ttt aag tgt      3739
226   Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu His Cys Phe Lys Cys
227           1000                1005                1010
228   gtt gcc tgt gag tgt gac ctc gga ggc tct tcc tca gga gct gaa gtc      3787
229   Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser Ser Gly Ala Glu Val
230   1015                1020                1025                1030
231   agg atc aga aac cac caa ctg tac tgc aac gac tgc tat ctc aga ttc      3835
232   Arg Ile Arg Asn His Gln Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe
233                       1035                1040                1045
234   aaa tct gga cgg cca acc gcc atg tga tgtaagcctc catacgaaag           3882
235   Lys Ser Gly Arg Pro Thr Ala Met  *
236                       1050
237   cactgttgca gatagaagaa gaggtggttg ctgctcatgt agatctataa atatgtgttg   3942
238   tatgtctttt ttgctttttt tttaaaaaaa agaataactt tttttgcctc tttagattac   4002
239   atagaagcat tgtagtcttg gtagaaccag tatttttgtt gtttatttat aaggtaattg   4062
240   tgtgtgggga aaagtgcagt atttacctgt tgaattcagc atcttgagag cacaagggaa   4122
```

VERIFICATION SUMMARY   DATE: 08/30/2004
PATENT APPLICATION: **US/10/763,692**   TIME: 14:40:10

Input Set : **N:\Crf3\RULE60\10763692.raw.txt**
Output Set: **N:\CRF4\08302004\J763692.raw**